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Minimum
Maximum
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Maximum Match 10
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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 PIR_66:*
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pir1:*
pir2:*
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25.057 Million cell updates/sec
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                                                                                                                                                            hypothetical prote
globulin1 - maize
vicilin-like stora
hypothetical prote
ATP-dependent RNA
probable RNA helic
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gene mastermind pr
hypothetical prote
vicilin like stora
globulin-1s, GLBIS
hypothetical prote
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alpha-globulin typ
protein PV100 [imp
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                                                                androgen receptor 
hypothetical prote
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hypothetical prote
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                                                                                                                                                                                                                                                                                                                                                                globulin-1
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                 receptor
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ALIGNMENTS

RESULT S22477

vicilin precursor -

cacao

17-Mar-1999

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alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: S08059
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germinat
A;Reference number: S06398
A;Accession: S08059
                                                                                                                                                                                                                                             RESULT
S08059
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: S22477; S22478; S18105; S22050
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C; Keywords: seed; storage protein
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A; Introns: 211/1; 269/3; 296/3; 391/3; 502/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-452 < MC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X62625
A;Accession: S22478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-566 < MCH>
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Plant Mol. Biol. 18, 1173-1176, 1992
A;Title: Comparison of the structure and 1
A;Reference number: S22477; MUID:92288309
A;Accession: S22477
A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1-24/Domain: signal sequence *status predicted <SIG>F;25-566/Product: vicilin *status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X62626
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Best Local S
Matches 28
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nes 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118.5; DB 2;
Pred. No. 4.4e-05;
4; Mismatches 17;
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                                                             and germination.
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                                                               XIX.
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R;Heck, G.R.; Chamberlain, A.K.; Ho, T.H.D. Mol. Gen. Genet. 239, 209-218, 1993
A;Title: Barley embryo globulin 1 gene, Begl: A;Reference number: S35221; MUID:93287988
                                                             C;Accession: S35221
R;Heck, G.R.; Chamberlain, A.K.;
                                                                                               globulin Beg1 precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994
                                                                                                                                                                                                                                        ₽
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F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #s
F;417/Binding site: carbohydrate (Asn) (covalent) #sta
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EWCNAB
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A; Residues: 1-509 <CI
C; Superfamily: glyci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; A;Experimental source: var. Coker 201 A;Experimental source: var. Coker 201 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 Plant Mol. Biol. 9, 533-546, 1987 Plant Mol. Developmental biochemistry of cottonseed embryogene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Mol. Biol. 7, 475-489, 1986
A;Title: Developmental biochemistry of cottonseed embryogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: A30838; S06911
R; Chlan, C.A.; Pyle, J.B.; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-globulin B precursor (clone C72) - upland cotton N;Alternate names: seed storage protein; vicilin precursor C;Species: Gossypium hirsutum (upland cotton) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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C;Comment: This is a seed storage protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-588 <CHL>
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                                                                                                                                                                                                                                                                              RGGS-----GRY--
                                                                                                                                                                                                                                                                                                                                                   DPQQREYEDCRRRCEQQEPRQQYQCQRRC----REQQ-----RQHGRGGDLINPQ 48
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                                                                                                                                                                                                                                      RKQQCVRECRERYQENPWRREREEEAEEEETEEGEQEQS 178
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9, 1986
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Pred. No. 4.6e-05;
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                                                                                                                                                                                                                                                                            -EEGEEKQS 63
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.00035;
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                                                                                                   21-Jul-2000
                       CDNA,
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                     chromosome mapp
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     Query Match
Best Local
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A; Map position: 4
C; Superfamily: glycinin
C; Keywords: glycoprotein
F; 174-190/Product: globulin
                                                                       R;Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura, J. Biol. Chem. 274, 2563-2570, 1999
A;Title: Multiple functional proteins are produced by cleaving Asn-G. A;Reference number: 222767; MUID:99107919
A;Accession: T44430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-globulin type A precursor - upland cotton
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar_1990 #sequence_revision 31-Mar-1990 #text_change
                                                                                                                                                                  protein PV100 [imported] - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change
C;Accession: T44430
                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted
F;25-605/Product: alpha-globulin type A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S06398
A;Accession: S06398
A;Status: not compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis
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   A; Cross-references: EMBL: AB019195;
                   A; Molecule type: mRNA
A; Residues: 1-810 < YAM>
                                                        A; Status: preliminary; translated
                                                                                                                                                                                                                                                T44430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-605 < CHL>
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A; Residues: 1-637 <HEC>
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Best Local
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                                                                                                                                                                                                                                                                                                                      DPQRR-YQDCRQHCQQEERRLRPHCEQSCREQ---
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20; Conserv
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                                                          from
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Pred. No. 0.
NID: g3808061; PIDN: BAA34056.1;
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                                                          GB/EMBL/DDBJ
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 PID: 93808062
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Similarity

25.4%;

Score Pred.

89.5; DB

<u>ب</u>

Length

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A;Cross-references: EMBL:X66247; NID:g3548; PIDN:CAA46973.1; PID:g3550 R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 10, 1363-1381, 1994 Yeast 10, 1363-1381, 1994 A;Title: Analysis of a 70 kb region on the right arm of yeast chromoson A;Reference number: S48255; MUID:95208357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Saccharomyces cerevisiae C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000 C:Accession: S25365; S48277; S45980; S25404; S25405; A30906; S44692 R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 8, 397-408, 1992
                                                                                                              A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55615.1; A;NOte: the nucleotide sequence was submitted to the EMBL Data R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I. submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-966 <MAW>
                                                                                                                                                                                                                                                                          A; Reference number: S48255; A; Accession: S48277
    A; Residues: 1-966 < A; Cross-references:
                       A; Molecule type: DNA
A; Residues: 1-966 <FE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Molecular analysis A; Reference number: $25364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYC8 protein - yeast (Saccharomyces cerevisiae) N.Alternate names: glucose repression mediator;
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                                                                      A; Accession: S45980
                                                                                              A; Reference number: S45927
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A;Molecule type: DNA
A;Residues: 1-236 <HILD
A;Residues: 1-236 <HILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Speciation and domestication in maize A;Reference number: Z14386; MUID:98429537 A;Accession: T01662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Hilton, H.; Gaut, B.S.
Genetics 150, 863-872, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              globulin-1 - maize (fragment)
C:Species: Zea mays (maize)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 11-Jan-2000
C:Accession: T01662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
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21; Conservative
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    EMBL: 235981;
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35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of yeast chromosome II between CMD1 and LYS2: the \mbox{\sc MUID:}\,92327848
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NID: g536449; PIDN: CAA85069.1;
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                                                                                                                                                                                                                                                                                                                     yeast chromosome
PID:9536450; MIPS:YBR112d
                                                                                                                                                           Library,
                                                                                                                                                                                 PID:g476068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SGD: CYC8; SSN6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S25405
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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Best Local
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les 19; Conserv
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hypothetical protein T01D1.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 C;Accession: T29475 R;Bradshaw, H.; Wohldmann, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Drive-selection equilibrium: homopolymer evolution A;Reference number: Z17850; MUID:94365848 A;Accession: T13998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: unassigned tetratricopeptide repeat proteins; C;Keywords: nucleus; transcription regulation F;224-257/Domain: tetratricopeptide repeat homology <TT1> F;262-295/Domain: tetratricopeptide repeat homology <TT2> F;266-299/Domain: tetratricopeptide repeat homology <TT3> F;296-329/Domain: tetratricopeptide repeat homology <TT3> F;365-398/Domain: tetratricopeptide repeat homology <TT5> F;365-398/Domain: tetratricopeptide repeat homology <TT5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:M92914; NID:g157833; PID:g157834; PIDN:AAC37201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Newfeld, S.J.; Tachida, H.; Yedvobnick, J. Mol. Evol. 38, 637-641, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene mastermind protein - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL:M23440; NID:g171349; PIDN:AAA34545.1;
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A; Residues: 1-546, 'K', 548-966 <TRU>
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Gene 73, 97-111, 1988
A;Title: Cloning and charact
A;Reference number: $25405;
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A; Residues: 1-546, 'K', 548-966 <SCH>
A; Cross-references: EMBL:M17826; NID:g172725;
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A;Title: Molecular analysis of SSN6, a gene
A;Reference number: S25404; MUID:88065502
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                                                                                                                                                                                                                           QQREYEDCRRRCEQQEPRQQYQCQRRCREQQRQH-----GRGGDLINPQRGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               required for complete derepression of ICL1; required for repression unassigned tetratricopeptide repeat proteins; tetratricopeptide repe
                                                                                                                                                                                                                                                                                                                                Conservative
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SGD:S0000316; MIPS:YBR112c
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                                                                                                                                                                                                                                                                                                                                                     22.2%;
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Pred. No. 1.7;
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0.57;
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C:Accession: A53234; A43642
R:Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A;Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene.
A;Reference number: A53234; MUID:92090707
A;Accession: A53234
                                                                                                                      globulin-15, GLBIS - maize
C;Species: Zea mays (maize)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
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A53234
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C;Species: Zea mays (maize)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000
C;Accession: S21825
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A; Residues: 1-540 < KRT>
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A;Introns: 25/3; 304/3
C;Superfamily: gliadin
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A;Experimental source: strain Bristol N2; clone T01D1
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A; Residues: 1-411 <BRA>
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A;Description: The sequence of C. elegans cosmid TOID1.
A;Reference number: Z20623
A;Accession: T29475
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Best Local Similarity 30.0%;
Matches 21; Conservative 1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                         59 EEKQ 62
                                                                                                                                                                                                                                                                                                                                                                                  40 CVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADD----RSGEGSSEDEREREQEK 94
                                                                                                                                                                                                                                                                                                                                                                                                                    12 CRRRCEQQEPRQQYQCQRRCRE-----QQRQHGRGGDLINPQRGGSG------RYEEG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 GRYEEGEEKQ 62
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Pred. No. 0.55;
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submitted to the EMBL Data Library, A:Reference number: Z20179 A;Accession: T26242
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A;Title: Characterization of embryo globulins encoded by the maize Glb genes.
A;Reference number: A43642; MUID:89374022
A;Accession: A43642.
                                                                                   submitted to the EMBL Data Library, December 1996 A; Reference number: Z20179 A; Accession: T26243
                                                                                                                                                                          C; Accession: T26243
                                                                                                                                                                                            hypothetical protein W06F12.2b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Cross-references: EMBL:Z83244; PIDN:CAB54315.1; GSPDB:GN00021; CESP:w06F12.2b
                      A; Molecule type: DNA
A; Residues: 1-568 <WIL>
                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                        R;Lloyd,
                                                                                                                                                                                                                                                                 T26243
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A; Residues: 1-562 <WIL>
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A; Residues: 1-573 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                       440
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 EEKQ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 EEKQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 CVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADD-----RSGEGSSEDEREREQEK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 CRRRCEQQEPRQQYQCQRRCRE-----QQRQHGRGGDLINPQRGGSG------RYEEG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                               1 KRDPQQREYEDCRRRCEQQEPRQQYQCQRRCREQQRQHGRGG--DLINPQRGG
                                                                                                                                                                                                                                                                                                                                                       ERERENRDNERGRRERESEAPRRRKEDDRRSRHQDSQEASGGSQEMSFPLSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75/1; 153/3; 201/1; 214/1; 283/1; 305/3; 332/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 2; pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 573,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                       492
                                                                                                                                                                                                                                                                                                                                                                                               51
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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globulin1 - maize

C:Species: Zea mays (maize)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 29-Oct-1999
C;Accession: T02258
R;Bhattramakki, D.; Kriz, A.L.
submitted to the EMBL Data Library, May 1995
A;Description: Nucleotide sequence analysis of a novel globulin1 null allele from the II
A;Reference number: Z14643
A;Accession: T02258
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-407 <BHA>
A;Residues: 1-407 <BHA>
A;Cross-references: EMBL:UZ8017; NID:g927238; PIDN:AAB60295.1; PID:g927239
A;Experimental source: strain IHP
C;Gene: Glb1
A;Introns: 168/1; 226/3; 254/1; 351/1
Search completed: March 1, 2001, 15:52:32 Job time: 556 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Experimental source: clone W06F12
C:Genetics:
A:Gene: CESP:W06F12.2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
T02258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 3
A; Introns: 23/3; 81/1; 159/3; 207/1; 220/1; 289/1; 311/3; 338/2; 561/3
                                                                                                                                                                                                                 Query Match 21.1%;
Best Local Similarity 31.6%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.2%; Score 75; DB 2; Length 568; Best Local Similarity 34.0%; Pred. No. 1.5; Matches 18; Conservative 10; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 ERERENRDNERGRRERESEAPRRRKEDDRRSRHQDSQEASGGSQEMSFPLSGG 498
                                                                                                                      40 CVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADD-----RSGKGSSEDERERE 91
                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                     Score 74.5; DB 2; Length 407; Pred, No. 1.3;
                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                 Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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